



ATTACHMENTS:

- 2) Computer readable copy of corrected Sequence Listing



ATTACHMENTS:

Mark-up of Sequence Listing as originally filed



SEQUENCE LISTING

*VERSION
SHOWING
CORRECTIONS*

<110> Sumitomo Chemical Co., Ltd

5

<120> PROCESS FOR PRODUCING OPTICALLY ACTIVE 4-HALO-3-HYDROXYBUTANOATE

<130>

10

<140>

<141>

<160> 27

15

<170> PatentIn Ver. 2.1

<210> 1

<211> 325

20 <212> PRT

<213> Penicillium citrinum

<400> 1

Met	Ser	Asn	Gly	Lys	Thr	Phe	Thr	Leu	Ser	Asn	Gly	Val	Lys	Ile	Pro
1															

25

15

Gly	Val	Gly	Phe	Gly	Thr	Phe	Ala	Ser	Glu	Gly	Ser	Lys	Gly	Glu	Thr

20

25

30

Tyr	Thr	Ala	Val	Thr	Thr	Ala	Leu	Lys	Thr	Gly	Tyr	Arg	His	Leu	Asp

30

35

40

45

Cys	Ala	Trp	Tyr	Tyr	Leu	Asn	Glu	Gly	Glu	Val	Gly	Glu	Ile	Arg

35

Asp	Phe	Leu	Lys	Glu	Asn	Pro	Ser	Val	Lys	Arg	Glu	Asp	Ile	Phe	Val

65

70

75

80

Cys	Thr	Lys	Val	Trp	Asn	His	Leu	His	Arg	Tyr	Glu	Asp	Val	Leu	Trp

40

85

90

95

Lys Asn Leu Ser Ala
325

5 <210> 2
 <211> 978
 <212> DNA
 <213> Penicillium citrinum

10 <220>
 <221> CDS
 <222> (1)..(978)

<400> 2
 15 atg tot aac gga aag act ttc aca ttg agc aac ggc gtc aag att cct 48
 Met Ser Asn Gly Lys Thr Phe Thr Leu Ser Asn Gly Val Lys Ile Pro
 1 5 10 15

20 ggc gtc ggc ttt ggt acc ttc gct agt gaa ggt tcc aag ggc gag acc 96
 Gly Val Gly Phe Gly Thr Phe Ala Ser Glu Gly Ser Lys Gly Glu Thr
 20 25 30

25 tat act gct gtc acc act gcc ctg aag acc ggt tac cgt cac ttg gac 144
 Tyr Thr Ala Val Thr Thr Ala Leu Lys Thr Gly Tyr Arg His Leu Asp
 35 40 45

30 tgt gcc tgg tac tac ctg aac gag ggt gag gtt ggt gag ggt atc cgt 192
 Cys Ala Trp Tyr Tyr Leu Asn Glu Gly Glu Val Gly Glu Ile Arg
 50 55 60

35 gac ttc ctg aag gag aac ccc tcg gtg aag cgt gag gac atc ttc gtc 240
 Asp Phe Leu Lys Glu Asn Pro Ser Val Lys Arg Glu Asp Ile Phe Val
 65 70 75 80

40 tgc acc aag gtg tgg aac cac ctc cac cgt tat gag gac gtc ctc tgg 288
 Cys Thr Lys Val Trp Asn His Leu His Arg Tyr Glu Asp Val Leu Trp
 85 90 95

45 tcc att gac gac tcc ctg aag cgt ctt gga ctt gac tac gtt gat atg 336
 Ser Ile Asp Asp Ser Leu Lys Arg Leu Gly Leu Asp Tyr Val Asp Met
 100 105 110

Ser Ile Asp Asp Ser Leu Lys Arg Leu Gly Leu Asp Tyr Val Asp Met
 100 105 110
 Phe Leu Val His Trp Pro Ile Ala Ala Glu Lys Asn Gly Gln Gly Glu
 5 115 120 125
 Pro Lys Ile Gly Pro Asp Gly Lys Tyr Val Ile Leu Lys Asp Leu Thr
 130 135 140
 10 Glu Asn Pro Glu Pro Thr Trp Arg Ala Met Glu Lys Ile Tyr Glu Asp
 145 150 155 160
 Arg Lys Ala Arg Ser Ile Gly Val Ser Asn Trp Thr Ile Ala Asp Leu
 165 170 175
 15 Glu Lys Met Ser Lys Phe Ala Lys Val Met Pro His Ala Asn Gln Ile
 180 185 190
 Glu Ile His Pro Phe Leu Pro Asn Glu Glu Leu Val Gln Tyr Cys Phe
 20 195 200 205
 Ser Lys Asn Ile Met Pro Val Ala Tyr Ser Pro Leu Gly Ser Gln Asn
 210 215 220
 25 Gln Val Pro Thr Thr Gly Glu Arg Val Ser Glu Asn Lys Thr Leu Asn
 225 230 235 240
 Glu Ile Ala Glu Lys Gly Gly Asn Thr Leu Ala Gln Val Leu Ile Ala
 245 250 255
 30 Trp Gly Leu Arg Arg Gly Tyr Val Val Leu Pro Lys Ser Ser Asn Pro
 260 265 270
 Lys Arg Ile Glu Ser Asn Phe Lys Ser Ile Glu Leu Ser Asp Ala Asp
 35 275 280 285
 Phe Glu Ala Ile Asn Ala Val Ala Lys Gly Arg His Phe Arg Phe Val
 290 295 300
 40 Asn Met Lys Asp Thr Phe Gly Tyr Asp Val Trp Pro Glu Glu Thr Ala
 305 310 315 320

	ttc ctc gtt cac tgg ccc att gct gcc gag aag aat ggc cag ggt gag	384
	Phe Leu Val His Trp Pro Ile Ala Ala Glu Lys Asn Gly Gln Gly Glu	
	115 120 125	
5	ccc aag att ggc cct gac ggc aaa tac gtc att ctc aag gac ctg acc	432
	Pro Lys Ile Gly Pro Asp Gly Lys Tyr Val Ile Leu Lys Asp Leu Thr	
	130 135 140	
10	gag aac ccc gag ccc aca tgg cgc gct atg gag aag att tat gag gat	480
	Glu Asn Pro Glu Pro Thr Trp Arg Ala Met Glu Lys Ile Tyr Glu Asp	
	145 150 155 160	
15	cgc aag gcc agg tcc att ggt gtc tcc aac tgg acc att gcc gac ctt	528
	Arg Lys Ala Arg Ser Ile Gly Val Ser Asn Trp Thr Ile Ala Asp Leu	
	165 170 175	
20	gag aag atg tcc aag ttc gcc aag gtc atg cct cac gcc aac cag atc	576
	Glu Lys Met Ser Lys Phe Ala Lys Val Met Pro His Ala Asn Gln Ile	
	180 185 190	
25	gag att cac ccc ttc ctg ccc aac gag gag ctg gtg cag tac tgc ttc	624
	Glu Ile His Pro Phe Leu Pro Asn Glu Glu Leu Val Gln Tyr Cys Phe	
	195 200 205	
30	tcc aag aac att atg ccc gtg gcc tac tct cct ctg ggc tcg cag aac	672
	Ser Lys Asn Ile Met Pro Val Ala Tyr Ser Pro Leu Gly Ser Gln Asn	
	210 215 220	
35	cag gtt ccc aco acc ggt gag cgg gtc agc gag aac aag act ctg aac	720
	Gln Val Pro Thr Thr Gly Glu Arg Val Ser Glu Asn Lys Thr Leu Asn	
	225 230 235 240	
40	gag atc gcc gag aag ggc ggc aac acc ctt gct cag gtt ctt att gcc	768
	Glu Ile Ala Glu Lys Gly Gly Asn Thr Leu Ala Gln Val Leu Ile Ala	
	245 250 255	
	tgg ggt ctg cgc cgt ggc tac gtc gtt ctc ccc aag agc tcc aac ccc	816
	Trp Gly Leu Arg Arg Gly Tyr Val Val Leu Pro Lys Ser Ser Asn Pro	
	260 265 270	
	aag cgc att gag tcc aac ttc aag agc att gag ctc tcc gat gcc gac	864
	Lys Arg Ile Glu Ser Asn Phe Lys Ser Ile Glu Leu Ser Asp Ala Asp	

275

280

285

912

ttt gaa gcc atc aat gcc gtt gcc aag ggt cgt cac ttc cgt ttc gtc
 Phe Glu Ala Ile Asn Ala Val Ala Lys Gly Arg His Phe Arg Phe Val

5 290

295

300

960

aac atg aag gat act ttc gga tat gat gtc tgg ccc gag gag acc gcc
 Asn Met Lys Asp Thr Phe Gly Tyr Asp Val Trp Pro Glu Glu Thr Ala
 305 310 315 320

10

aag aac ctg tct gcg tga
 Lys Asn Leu Ser Ala
 325

978

15

<210> 3
 <211> 17
 <212> PRT
 <213> Penicillium citrinum

20

<400> 3
 Asn Ile Met Pro Val Ala Tyr Ser Pro Leu Gly Ser Gln Asn Gln Val
 1 5 10 15

25 Pro

<210> 4
 30 <211> 10
 <212> PRT
 <213> Penicillium citrinum

<400> 4
 35 Ile Pro Gly Val Phe Gly Thr Phe Ala Ser
 1 5 10

<210> 5
 40 <211> 17
 <212> PRT
 <213> Penicillium citrinum

<400> 5

Ser Ile Glu Leu Ser Asp Ala Asp Phe Glu Ala Ile Asn Ala Val Ala
1 5 10 15

5

Lys

10 <210> 6

<211> 14

<212> PRT

<213> Penicillium citrinum

15 <400> 6

Met Ile Gly Val Ala Asn Tyr Thr Ile Ala Asp Leu Glu Lys

1 5 10

20 <210> 7

<211> 14

<212> PRT

<213> Penicillium citrinum

25 <400> 7

Tyr Glu Asp Val Leu Xaa Xaa Ile Asp Asp Ser Leu Lys Arg

1 5 10

30 <210> 8

<211> 20

<212> DNA

<213> Artificial Sequence

35 <220>

<223> Description of Artificial Sequence: Designed
oligonucleotide primer for PCR

<400> 8

40 ggaacytgrt tytgswacc

20

<210> 9
<211> 20
<212> DNA
<213> Artificial Sequence

5 <220>
<223> Description of Artificial Sequence:Designed
oligonucleotide primer for PCR

10 <400> 9 tangcnacng goataatatt 20

15 <210> 10
<211> 20
<212> DNA
<213> Artificial Sequence

20 <220>
<223> Description of Artificial Sequence:Designed
oligonucleotide primer for PCR

25 <400> 10 tangcnacng gcataatgtt 20

25 <210> 11
<211> 20
<212> DNA
<213> Artificial Sequence

35 <220>
<223> Description of Artificial Sequence:Designed
oligonucleotide primer for PCR

35 <400> 11 tangcnacng gcatgatatt 20

40 <210> 12
<211> 20
<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Designed
5 oligonucleotide primer for PCR

<400> 12

tangcnacng gcatgatgtt

20

10

<210> 13

<211> 20

<212> DNA

<213> Artificial Sequence

15

<220>

<223> Description of Artificial Sequence:Designed
oligonucleotide primer for PCR

20 <400> 13

tangcnacng gcattatatt

20

25 <210> 14

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

30 <223> Description of Artificial Sequence:Designed
oligonucleotide primer for PCR

35 <400> 14

tangcnacng gcattatgtt

20

40 <210> 15

<211> 697

<212> DNA

<213> Escherichia coli

<400> 15

cgctctaaaa ctantggatc ccccggtctg caggaattcg gcggcgogg atccaacgga 60
 aanacttca cactgagcaa cggcgtcaaa attcctggcg tcggctttgg tacotncgct 120
 agtgaagggtt ccaagggcga aacctatnct gctgtcacca ctgcctgaa aaccggttac 180
 cgtcncttgg actgtgcctg gtactacctg aacaagggtg aggttgtga gggtnccgt 240
 5 gacttcctga aggaaaaccc ctgggtgaag cgtgaggaca tcttcgtctg caccaaggta 300
 tggaaccacc tccaccgtta tgaggacgtc ctctggtcca ttgacnactc cctgaagcgt 360
 ctggacttg actacgttga tatgttcctc gttcaactggc ccattgctgc cgaaaaaaaaat 420
 ggccagggtg agccaaaaat tggccctgac ggcaaatacn tcnttctcaa ggacctgacc 480
 gaaaancccna ncccacctgg cgcgctatgg aaaaaatttn tgangateccc aaggccaggt 540
 10 ccattggtgt ttccaaattgg accattgccg accttgagaa gatgtccaag ttngccaagg 600
 tnatgcctca cgccaaaccag atcgagatc accccttcct gcccaacgag gagctgggtc 660
 agtactgctt ttccaaagaac antatgcccc tagcgta 697

15 <210> 16
 <211> 21
 <212> DNA
 <213> Artificial Sequence

20 <220>
 <223> Description of Artificial Sequence: Designed
 oligonucleotide primer for PCR

<400> 16
 25 ggaggtggtt ccacaccttg g 21

<210> 17
 <211> 20
 30 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Designed
 35 oligonucleotide primer for PCR

<400> 17
 caaccagatc gagattcacc 20

40 <210> 18
 <211> 331

<212> DNA

<213> Escherichia coli

<400> 18

5 cgctotaaaa ctantggatc ccccgggctg caggaattcg goggccgcgg atccttcata 60
 cccatcatgt ctaacggaaa gactttcaca ttgagcaacg gcgtcaagat tcctggcgta 120
 ggcttggta ccttcgttag tgaaggttcc aaggcgaga cctatactgc tgtcaccact 180
 gccctgaaga ccgggttaccg tcacttggac tgtcctgggt actacctgaa cgagggtgag 240
 gtgggtgagg gtatccgtga cttccctgaag gagaacccct cggtaagcg tgaggacatc 300
 10 ttcgtctgca ccaaggtgtg gaaccacatc c 331

<210> 19

<211> 743

<212> DNA

<213> Escherichia coli

<400> 19

20 caaccagatc gagattcacc ctttcctgco caacgaggag ctgggtcagt actgcttctc 60
 caagaacatt atgcccgtgg cctactctcc tctgggctcg cagaaccagg ttcccaccac 120
 cggtgagcgg gtcagcgaga acaagactct gaacgagatc gccgagaagg gcccgaacac 180
 ccttgcctcg gtttttattt cctggggctt gcggcgtggc tacgtcgat tccccaaagag 240
 ctccaacccc aagcgattt agtccaaactt caagagcatt gagctctcg atgcccactt 300
 tgaaggccatc aatggccattt ccaagggtcg tcacttccgt ttgtcaaca tgaaggatac 360
 25 tttcgatat gatgtctggc ccgaggagac cgccaagaac ctgtctcgat gaatctctac 420
 gaaattataa aatnacaccn acnaaaancc aaagcgaaag gatgatncc aaaantttt 480
 agggtttctt gtttgaaaac gtttattgan cccgaantga angaatagat gancntgatt 540
 tctccaaaaaa aaaaaaaaaa aaaaacggtc cgccggccgtt ccnnnggggg gcccgggttcc 600
 caattcnccc cttatnattt aattctttt taanggggncc aaattccncc nnatttccnt 660
 30 cnanattggn nggccgcctc caaactttcn tcntnaaagg gncccaattc ccccccnatt 720
 aantggattt cctntttacc ttt 743

<210> 20

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

40 <223> Description of Artificial Sequence:Designed
 oligonucleotide primer for PCR

<400> 20

ccaagggtgtg gaaccaccc tc

21

5 <210> 21

<211> 21

<212> DNA

<213> Artificial Sequence

10 <220>

<223> Description of Artificial Sequence:Designed
oligonucleotide primer for PCR

<400> 21

15 ccagaggaga gtagggccacg g

21

<210> 22

<211> 417

20 <212> DNA

<213> Escherichia coli

<400> 22

ccaagggtgtg gaaccaccc caccgttatg aggacgtcct ctggccatt gacgactccc 60

25 tgaagcgtct tggacttgac tacgttgata tgccctcggt tcactggccc attgctgccg 120

agaagaatgg ccagggtgag ccoaagattt ggcctgacgg caaaatacgcc attctcaagg 180

acctgaccga gaaccccgag cccacatggc ggcctatggg gaagattttt gaggatcgca 240

aggccagggtc cattgggtgc tccaaactggc ccattgcccga ccttgagaag atgtccaagt 300

tcgccaagggt catgcctcac gccaaccaga tcgagattca ccccttccgt cccaaacgagg 360

30 agctggtgca gtactgcttc tccaaagaaca ttatgcccgt ggcctactct cctctgg 417

<210> 23

<211> 27

35 <212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Designed
oligonucleotide primer for PCR

<400> 23

gccccatggctta tgtcttaacgg aaagact

27

<210> 24

5 <211> 29

<212> DNA

<213> Artificial Sequence

<220>

10 <223> Description of Artificial Sequence:Designed
oligonucleotide primer for PCR

<400> 24

cggatccgtt ataatttcgt agagattca

29

15

<210> 25

<211> 21

<212> DNA

20 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Designed
oligonucleotide primer for PCR

25

<400> 25

gatcatcata gcaggaggatca t

21

30 <210> 26

<211> 21

<212> DNA

<213> Artificial Sequence

35 <220>

<223> Description of Artificial Sequence:Designed
oligonucleotide primer for PCR

<400> 26

40 gaattcaaca ccagttagct c

21

<210> 27
 <211> 786
 <212> DNA
 <213> Escherichia coli

5

<220>
 <221> CDS
 <222> (1)..(786)

10 <400> 27

atg tat aaa gat tta gaa gga aaa gta gtt gtc ata aca ggt tca tct 48
 Met Tyr Lys Asp Leu Glu Gly Lys Val Val Val Ile Thr Gly Ser Ser
 1 5 10 15

15 acc ggt tta gga aaa gca atg gcg att cgt ttt gcg aca gaa aaa gct 96
 Thr Gly Leu Gly Lys Ala Met Ala Ile Arg Phe Ala Thr Glu Lys Ala
 20 25 30

20 aaa gta gtt gtg aac tat cgt tcg aaa gaa gaa gct aac agc gtt 144
 Lys Val Val Asn Tyr Arg Ser Lys Glu Glu Ala Asn Ser Val
 35 40 45

25 tta gaa gaa att aaa aaa gtg ggc gga gag gct att gcc gtc aaa ggt 192
 Leu Glu Glu Ile Lys Lys Val Gly Gly Glu Ala Ile Ala Val Lys Gly
 50 55 60

30 gat gta aca gtt gag tct gat gtg atc aat tta gtt caa tct gct att 240
 Asp Val Thr Val Glu Ser Asp Val Ile Asn Leu Val Gln Ser Ala Ile
 65 70 75 80

35 aaa gaa ttt gga aag cta gac gtt atg att aat aac gca gga atg gaa 288
 Lys Glu Phe Gly Lys Leu Asp Val Met Ile Asn Asn Ala Gly Met Glu
 85 90 95

40 aat ccg gtt tcg tct cat gaa atg tct tta agt gat tgg aat aaa gtc 336
 Asn Pro Val Ser Ser His Glu Met Ser Leu Ser Asp Trp Asn Lys Val
 100 105 110

45 att gat acg aac tta acg gga gca ttt tta ggc ago cgt gaa gcg att 384
 Ile Asp Thr Asn Leu Thr Gly Ala Phe Leu Gly Ser Arg Glu Ala Ile
 115 120 125

	aaa tat ttt gtg gaa aat gat att aag gga aca gtt att aac atg tcg	432
	Lys Tyr Phe Val Glu Asn Asp Ile Lys Gly Thr Val Ile Asn Met Ser	
	130 135 140	
5	agt gtt cac gag aaa att cct tgg cca tta ttt gtt cat tac gca gca	480
	Ser Val His Glu Lys Ile Pro Trp Pro Leu Phe Val His Tyr Ala Ala	
	145 150 155 160	
10	agt aaa ggc gga atg aag ctc atg acc gaa aca ctt gca tta gaa tac	528
	Ser Lys Gly Gly Met Lys Leu Met Thr Glu Thr Leu Ala Leu Glu Tyr	
	165 170 175	
15	gct cca aaa ggt att cgt gta aat aac att gga ccg gga gcg att aat	576
	Ala Pro Lys Gly Ile Arg Val Asn Asn Ile Gly Pro Gly Ala Ile Asn	
	180 185 190	
20	aca ccg att aac gct gag aaa ttt gct gat cct gag cag cgt gca gat	624
	Thr Pro Ile Asn Ala Glu Lys Phe Ala Asp Pro Glu Gln Arg Ala Asp	
	195 200 205	
25	gta gaa agc atg att cca atg gga tac att gga gag ccg gaa gaa att	672
	Val Glu Ser Met Ile Pro Met Gly Tyr Ile Gly Glu Pro Glu Glu Ile	
	210 215 220	
30	gca gcg gtt gct gca tgg cta gct tct tca gag gca agt tat gta aca	720
	Ala Ala Val Ala Ala Trp Leu Ala Ser Ser Glu Ala Ser Tyr Val Thr	
	225 230 235 240	
35	caa gca gga cgc gga taa	786
	Gln Ala Gly Arg Gly	
	260	
40	<210> 28 <211> 996 <212> DNA <213> Penicillium citrinum	

220

<221> CDS

<222> (1)..(978)

	Glu Asn Pro Glu Pro Thr Trp Arg Ala Met Glu Lys Ile Tyr Glu Asp		
145	150	155	160
5	cgc aag gcc agg tcc att ggt gtc tcc aac tgg acc att gcc gac ctt Arg Lys Ala Arg Ser Ile Gly Val Ser Asn Trp Thr Ile Ala Asp Leu		528
	165	170	175
10	gag aag atg tcc aag ttc gcc aag gtc atg cct cac gcc aac cag atc Glu Lys Met Ser Lys Phe Ala Lys Val Met Pro His Ala Asn Gln Ile		576
	180	185	190
15	gag att cac ccc ttc ctg ccc aac gag gag ctg gtg cag tac tgc ttc Glu Ile His Pro Phe Leu Pro Asn Glu Glu Leu Val Gln Tyr Cys Phe		624
	195	200	205
	tcc aag aac att atg ccc gtg gcc tac tct cct ctg ggc tcg cag aac Ser Lys Asn Ile Met Pro Val Ala Tyr Ser Pro Leu Gly Ser Gln Asn		672
	210	215	220
20	cag gtt ccc acc acc ggt gag cgg gtc agc gag aac aag act ctg aac Gln Val Pro Thr Thr Gly Glu Arg Val Ser Glu Asn Lys Thr Leu Asn		720
	225	230	235
25	240		
	gag atc gcc gag aag ggc ggc aac acc ctt gct cag gtt ctt att gcc Glu Ile Ala Glu Lys Gly Gly Asn Thr Leu Ala Gln Val Leu Ile Ala		768
	245	250	255
30	tgg ggt ctg cgc cgt ggc tac gtc gtt ctc ccc aag agc tcc aac ccc Trp Gly Leu Arg Arg Gly Tyr Val Val Leu Pro Lys Ser Ser Asn Pro		816
	260	265	270
35	aag cgc att gag tcc aac ttc aag agc att gag ctc tcc gat gcc gac Lys Arg Ile Glu Ser Asn Phe Lys Ser Ile Glu Leu Ser Asp Ala Asp		864
	275	280	285
40	ttt gaa gcc atc aat gcc gtt gcc aag ggt cgt cac ttc cgt ttc gtc Phe Glu Ala Ile Asn Ala Val Ala Lys Gly Arg His Phe Arg Phe Val		912
	290	295	300
	aac atg aag gat act ttc gga tat gat gtc tgg ccc gag gag acc gcc Asn Met Lys Asp Thr Phe Gly Tyr Asp Val Trp Pro Glu Glu Thr Ala		960
	305	310	315
			320

aag aac ctg tct gcg tga atctctacga aattataa	996
Lys Asn Leu Ser Ala	
325	
5	
<210> 29	
<211> 29	
<212> DNA	
<213> Artificial Sequence	
10	
<220>	
<223> Description of Artificial Sequence Designed oligonucleotide primer for PCR	
15	
<400> 29	
cggatccgtt cacgcagaca ggttcttgg	29
20	
<210> 30	
<211> 978	
<212> DNA	
<213> Penicillium citrinum	
25	
<220>	
<221> CDS	
<222> (1).. (978)	
30	
<400> 30	
atg tct aac gga aag act ttc aca ttg agc aac ggc gtc aag att cct	48
Met Ser Asn Gly Lys Thr Phe Thr Leu Ser Asn Gly Val Lys Ile Pro	
1 5 10 15	
35	
ggc gtc ggc ttt ggt acc ttc got agt gaa ggt tcc aag ggc gag acc	96
Gly Val Gly Phe Gly Thr Phe Ala Ser Glu Gly Ser Lys Gly Glu Thr	
20 25 30	
40	
tat act gct gtc acc act gcc ctg aag acc ggt tac cgt cac ttg gag	144
Tyr Thr Ala Val Thr Thr Ala Leu Lys Thr Gly Tyr Arg His Leu Asp	
35 40 45	
45	
tgt gcc tgg tac tac ctg aac gag ggt gag gtt ggt gag ggt atc cgt	192
Cys Ala Trp Tyr Tyr Leu Asn Glu Gly Glu Val Gly Glu Gly Ile Arg	
50 55 60	

	gac ttc ctg aag gag aac ccc tcg gtg aag cgt gag gac atc ttc gtc	240		
	Asp Phe Leu Lys Glu Asn Pro Ser Val Lys Arg Glu Asp Ile Phe Val			
65	65	70	75	80
5	tgc acc aag gtg tgg aac cac ctc cac cgt tat gag gac gtc ctc tgg	288		
	Cys Thr Lys Val Trp Asn His Leu His Arg Tyr Glu Asp Val Leu Trp			
	85	90	95	
10	tcc att gac gac tcc ctg aag cgt ctt gga ctt gac tac gtt gat atg	336		
	Ser Ile Asp Asp Ser Leu Lys Arg Leu Gly Leu Asp Tyr Val Asp Met			
	100	105	110	
15	ttc ctc gtt cac tgg ccc att gct gcc gag aag aat ggc cag ggt gag	384		
	Phe Leu Val His Trp Pro Ile Ala Ala Glu Lys Asn Gly Gln Gly Glu			
	115	120	125	
20	ccc aag att ggc cct gac ggc aaa tac gtc att ctc aag gac ctg acc	432		
	Pro Lys Ile Gly Pro Asp Gly Lys Tyr Val Ile Leu Lys Asp Leu Thr			
	130	135	140	
25	gag aac ccc gag ccc aca tgg cgc gct atg gag aag att tat gag gat	480		
	Glu Asn Pro Glu Pro Thr Trp Arg Ala Met Glu Lys Ile Tyr Glu Asp			
	145	150	155	160
	cgc aag gcc agg tcc att ggt gtc tcc aac tgg acc att gcc gac ctt	528		
	Arg Lys Ala Arg Ser Ile Gly Val Ser Asn Trp Thr Ile Ala Asp Leu			
	165	170	175	
30	gag aag atg tcc aag ttc gcc aag gtc atg cct cac gcc aac cag atc	576		
	Glu Lys Met Ser Lys Phe Ala Lys Val Met Pro His Ala Asn Gln Ile			
	180	185	190	
35	gag att cac ccc ttc ctg ccc aac gag gag ctg gtg cag tac tgc ttc	624		
	Glu Ile His Pro Phe Leu Pro Asn Glu Glu Leu Val Gln Tyr Cys Phe			
	195	200	205	
40	tcc aag aac att atg ccc gtg gcc tac tct cct ctg ggc tcg cag aac	672		
	Ser Lys Asn Ile Met Pro Val Ala Tyr Ser Pro Leu Gly Ser Gln Asn			
	210	215	220	
	cag gtt ccc acc acc ggt gag cgg gtc agc gag aac aag act ctg aac	720		

	Gln Val Pro Thr Thr Gly Glu Arg Val Ser Glu Asn Lys Thr Leu Asn		
225	230	235	240
5	gag atc gcc gag aag ggc ggc aac acc ctt gct cag gtt ctt att gcc Glu Ile Ala Glu Lys Gly Gly Asn Thr Leu Ala Gln Val Leu Ile Ala		768
	245	250	255
10	tgg ggt ctg cgc cgt ggc tac gtc gtt ctc ccc aag agc tcc aac ccc Trp Gly Leu Arg Arg Gly Tyr Val Val Leu Pro Lys Ser Ser Asn Pro		816
	260	265	270
15	aag cgc att gag tcc aac ttc aag agc att gag ctc tcc gat gcc gac Lys Arg Ile Glu Ser Asn Phe Lys Ser Ile Glu Leu Ser Asp Ala Asp		864
	275	280	285
20	ttt gaa gcc atc aat gcc gtt gcc aag ggt cgt cac ttc cgt ttc gtc Phe Glu Ala Ile Asn Ala Val Ala Lys Gly Arg His Phe Arg Phe Val		912
	290	295	300
25	aag aac ctg tot gcg tga Lys Asn Leu Ser Ala		978
	325		
30	<210> 31 <211> 27 <212> DNA <213> Artificial Sequence		
35	<220> <223> Description of Artificial Sequence Designed oligonucleotide primer for PCR		
40	<400> 31 gccccatggctta tgtataaaga ttttagaa	27	
	<210> 32 <211> 23		

<212> DNA

<213> Artificial Sequence

<220>

5 <223> Description of Artificial Sequence Designed oligonucleotide primer
for PCR

<400> 32

cggatccgtt atccgcgtcc tgc

23

10

<210> 33

<211> 28

<212> DNA

<213> Artificial Sequence

15

<220>

<223> Description of Artificial Sequence Designed oligonucleotide primer
for PCR

20 <400> 33

cggatccgag cgcccaatac gcaaaccg

28

<210> 34

<211> 385

25 <212> PRT

<213> Corynebacterium sp.

<400> 34

Met Lys Ala Ile Gln Tyr Thr Arg Ile Gly Ala Glu Pro Glu Leu Thr

30 1 5 10 15

Glu Ile Pro Lys Pro Glu Pro Gly Pro Gly Glu Val Leu Leu Glu Val
20 25 3035 Thr Ala Ala Gly Val Cys His Ser Asp Asp Phe Ile Met Ser Leu Pro
35 40 45Glu Glu Gln Tyr Thr Tyr Gly Leu Pro Leu Thr Leu Gly His Glu Gly
50 55 60

Ala Gly Lys Val Ala Ala Val Gly Glu Gly Val Glu Gly Leu Asp Ile
 65 70 75 80

5 Gly Thr Asn Val Val Val Tyr Gly Pro Trp Gly Cys Gly Asn Cys Trp
 85 90 95

His Cys Ser Gln Gly Leu Glu Asn Tyr Cys Ser Arg Ala Gln Glu Leu
 100 105 110

10 Gly Ile Asn Pro Pro Gly Leu Gly Ala Pro Gly Ala Leu Ala Glu Phe
 115 120 125

Met Ile Val Asp Ser Pro Arg His Leu Val Pro Ile Gly Asp Leu Asp
 15 130 135 140

Pro Val Lys Thr Val Pro Leu Thr Asp Ala Gly Leu Thr Pro Tyr His
 145 150 155 160

20 Ala Ile Lys Arg Ser Leu Pro Lys Leu Arg Gly Gly Ser Tyr Ala Val
 165 170 175

Val Ile Gly Thr Gly Gly Leu Gly His Val Ala Ile Gln Leu Leu Arg
 180 185 190

25 His Leu Ser Ala Ala Thr Val Ile Ala Leu Asp Val Ser Ala Asp Lys
 195 200 205

Leu Glu Leu Ala Thr Lys Val Gly Ala His Glu Val Val Leu Ser Asp
 30 210 215 220

Lys Asp Ala Ala Glu Asn Val Arg Lys Ile Thr Gly Ser Gln Gly Ala
 225 230 235 240

35 Ala Leu Val Leu Asp Phe Val Gly Tyr Gln Pro Thr Ile Asp Thr Ala
 245 250 255

Met Ala Val Ala Gly Val Gly Ser Asp Val Thr Ile Val Gly Ile Gly
 40 260 265 270

Asp Gly Gln Ala His Ala Lys Val Gly Phe Phe Gln Ser Pro Tyr Glu
 275 280 285

Ala Ser Val Thr Val Pro Tyr Trp Gly Ala Arg Asn Glu Leu Ile Glu
 290 295 300

5 Leu Ile Asp Leu Ala His Ala Gly Ile Phe Asp Ile ^{Ser Val Glu Thr}
 305 310 315 320
~~Phe Ser Leu Asp Asn Glu Ala Glu Ala Thr Arg Arg Leu Ala Ala Glu~~
~~Leu Gln Ser Arg Gln Arg Cys Arg Ser Val Ser Thr Thr Gly Cys Arg~~
 325 330 335

10 ~~Thr Leu Ser Glu Arg Ala Val Val Leu Pro Glu Leu~~
~~Asn Ala Gln Arg Pro Cys Gly Oys Gly Pro Trp Ser Val Val Pro Thr~~
 340 345 350

15 ~~Ala Val Glu Arg Gln Arg Lys Asn Thr Asp Ala Arg Pro Asn Ser Ile~~
 355 360 365

~~Arg Pro Gly Ile Ser Val Arg Asn Ser Val Cys Ala Ser Cys Thr Pro~~
 370 375 380

20 Arg
 385

<210> 35

25 <211> 1158

<212> DNA

<213> Corynebacterium sp.

30 <220>
 <221> CDS
 <222> (1).. (1158)

35 <400> 35
 atg aag gcg atc cag tac acg ^aga atc ggc gcg gaa ccc gaa ctc acg 48
 Met Lys Ala Ile Gln Tyr Thr Arg Ile Gly Ala Glu Pro Glu Leu Thr
 1 5 10 15

40 gag att ccc aaa ccc gag ccc ggt cca ggt gaa gtg ctc ctg gaa gtc 96
 Glu Ile Pro Lys Pro Glu Pro Gly Pro Gly Glu Val Leu Leu Glu Val
 20 25 30

acc gct gct ggc gtc tgc cac tcg gac gac ttc atc atg agc ctg ccc 144

	Thr Ala Ala Gly Val Cys His Ser Asp Asp Phe Ile Met Ser Leu Pro			
	35	40	45	
5	gaa gag cag tac acc tac ggc ctt ccg ctc acg ctc ggc cac gaa ggc Glu Glu Gln Tyr Thr Tyr Gly Leu Pro Leu Thr Leu Gly His Glu Gly		192	
	50	55	60	
10	gca ggc aag gtc gcc gcc gtc ggc gag ggt gtc gaa ggt ctc gac atc Ala Gly Lys Val Ala Ala Val Gly Glu Gly Val Glu Gly Leu Asp Ile		240	
	65	70	75	80
15	gga acc aat gtc gtc gtc tac ggg cct tgg ggt tgc ggc aac tgt tgg Gly Thr Asn Val Val Val Tyr Gly Pro Trp Gly Cys Gly Asn Cys Trp		288	
	85	90	95	
20	cac tgc tca caa gga ctc gag aac tat tgc tct cgc gcc caa gaa ctc His Cys Ser Gln Gly Leu Glu Asn Tyr Cys Ser Arg Ala Gln Glu Leu		336	
	100	105	110	
25	gga atc aat cct ccc ggt ctc ggt gca ccc ggc gcg ttg gcc gag ttc Gly Ile Asn Pro Pro Gly Leu Gly Ala Pro Gly Ala Leu Ala Glu Phe		384	
	115	120	125	
30	atg atc gtc gat tct cct cgc cac ctt gtc ccg atc ggt gac ctc gac Met Ile Val Asp Ser Pro Arg His Leu Val Pro Ile Gly Asp Leu Asp		432	
	130	135	140	
35	ccg gtc aag acg gtg ccg ctg acc gac gcc ggt ctg acg ccg tat cac Pro Val Lys Thr Val Pro Leu Thr Asp Ala Gly Leu Thr Pro Tyr His		480	
	145	150	155	160
40	gcg atc aag cgt tct ctg ccg aaa ctt cgc gga ggc tcg tac gcg gtt Ala Ile Lys Arg Ser Leu Pro Lys Leu Arg Gly Gly Ser Tyr Ala Val		528	
	165	170	175	
	180	185	190	
	195	200	205	

ctc gaa ctg gca acc aag gta ggc gct cac gaa gtg gtt ctg tcc gac 672
 Leu Glu Leu Ala Thr Lys Val Gly Ala His Glu Val Val Leu Ser Asp
 210 215 220

5
 aag gac gcg gcc gag aac gtc cgc aag atc act gga agt caa ggo gcc 720
 Lys Asp Ala Ala Glu Asn Val Arg Lys Ile Thr Gly Ser Gln Gly Ala
 225 230 235 240

10 gca ttg gtt ctc gac ttc gtc ggc tac cag ccc acc atc gac acc gcg 768
 Ala Leu Val Leu Asp Phe Val Gly Tyr Gln Pro Thr Ile Asp Thr Ala
 245 250 255

15 atg gct gtc gcc ggc gtc gga tca gac gtc acg atc gtc ggg atc ggg 816
 Met Ala Val Ala Gly Val Gly Ser Asp Val Thr Ile Val Gly Ile Gly
 260 265 270

20 gac ggc cag gcc cac gcc aaa gtc ggg ttc ttc caa agt cct tac gag 864
 Asp Gly Gln Ala His Ala Lys Val Gly Phe Phe Gln Ser Pro Tyr Glu
 275 280 285

25 gct tcg gtg aca gtc^c cog tat tgg ggt gcc cgc aac gag ttg atc gaa 912
 Ala Ser Val Thr Val Pro Tyr Trp Gly Ala Arg Asn Glu Leu Ile Glu
 290 295 300

30 ttg atc gac ctc gcc cac gcc ggc atc ttc gac atc ggc^{+ Ser} gtc gga gac 960
 Leu Ile Asp Leu Ala His Ala Gly Ile Phe Asp Ile Gly Gly Asp
 305 310 315 320

35 ctt cag tct cga caa cgg tgc cga agc gta tcg acg act ggc tgc cgg 1008
 Leu Gln Ser Arg Gln Arg Cys Arg Ser Val Ser Thr Thr Gly Cys Arg
 325 330 335

40 aac gct cag cgg ccg tgc ggt tgt ggt ccc tgg tct gta gta eeg aea 1056
 Asn Ala Gln Arg Pro Cys Gly Cys Gly Pro Trp Ser Val Val Pro Thr
 340 345 350

45 gcg gta gaa cga cag cgg aaa aac act gat gcc cgg ccg aat tcg att 1104
 Ala Val Glu Arg Gln Arg Lys Asn Thr Asp Ala Arg Pro Asn Ser Ile
 355 360 365

50 cgg ccg ggc atc agt gtc aga aat tcg gtg tgc got ago tgc aeg cct 1152

01年12月04日(火) 10時10分 完成 F E T F

発信:住友化学知的財産センター(株)

R:698

P.02/14

~~Arg Pro Gly Ile Ser Val Arg Asn Ser Val Cys Ala Ser Cys Thr Pro~~
370 375 380

~~cga tga~~

1158

5 Arg
385